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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/249,003**

DATE: 04/28/1999  
TIME: 14:55:13

**INPUT SET: S31648.raw**

**This Raw Listing contains the General Information Section and up to the first 5 pages.**

**SEQUENCE LISTING**

(1) General Information:

(i) APPLICANT: Wilson, Peter J  
Morris, Charles P  
Anson, Donald S  
Occhiodoro, Teresa  
Bielicki, Julie  
Clements, Peter R  
Hopwood, John J

**ENTERED**

(ii) TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF IDURONATE 2-SULFATASE

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Scully, Scott, Murphy & Presser  
21 (B) STREET: 400 Garden City Plaza  
22 (C) CITY: Garden City  
23 (D) STATE: New York  
24 (E) COUNTRY: USA  
25 (F) ZIP: 11530

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/249,003  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/991,973  
(B) FILING DATE: 17-DEC-1992

(viii) ATTORNEY/AGENT INFORMATION:

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PATENT APPLICATION US/09/249,003**DATE: 04/28/1999  
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47  
48       (A) NAME: DiGiglio, Frank S  
49       (B) REGISTRATION NUMBER: 31,346  
50       (C) REFERENCE/DOCKET NUMBER: 8416Z  
51

52       (ix) TELECOMMUNICATION INFORMATION:

53  
54       (A) TELEPHONE: 516-742-4343  
55       (B) TELEFAX: 516-742-4366  
56       (C) TELEX: 230 901 SANS UR  
57

58       (2) INFORMATION FOR SEQ ID NO:1:

59       (i) SEQUENCE CHARACTERISTICS:

60  
61       (A) LENGTH: 2297 base pairs  
62       (B) TYPE: nucleic acid  
63       (C) STRANDEDNESS: double  
64       (D) TOPOLOGY: linear  
65  
66

67       (ii) MOLECULE TYPE: cDNA  
68

69       (ix) FEATURE:

70  
71       (A) NAME/KEY: CDS  
72       (B) LOCATION: 125..1774  
73

74       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
75

76       CGGCTGTGTT GCGCAGTCCTT CATGGGTTCC CGACGAGGAG GTCTCTGTGG CTGCGGCCGC	60
77	
78       TGCTAACTGC GCCACCTGCT GCAGCCTGTC CCCGCCGCTC TGAAGCGGCC GCGTCGAAGC	120
79	
80       CGAA ATG CCG CCA CCC CGG ACC GGC CGA GGC CTT CTC TGG CTG GGT CTG	169
81       Met Pro Pro Pro Arg Thr Gly Arg Gly Leu Leu Trp Leu Gly Leu	
82            1            5            10            15	
83	
84       GTT CTG AGC TCC GTC TGC GCC CTC GGA TCC GAA ACG CAG GCC AAC	217
85       Val Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn	
86            20            25            30	
87	
88       TCG ACC ACA GAT GCT CTG AAC GTT CTT CTC ATC ATC GTG GAT GAC CTG	265
89       Ser Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu	
90            35            40            45	
91	
92       CGC CCC TCC CTG GGC TGT TAT GGG GAT AAG CTG GTG AGG TCC CCA AAT	313
93       Arg Pro Ser Leu Gly Cys Tyr Gly Asp Lys Leu Val Arg Ser Pro Asn	
94            50            55            60	
95	
96       ATT GAC CAA CTG GCA TCC CAC AGC CTC CTC TTC CAG AAT GCC TTT GCG	361
97       Ile Asp Gln Leu Ala Ser His Ser Leu Leu Phe Gln Asn Ala Phe Ala	
98            65            70            75	
99	

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100	CAG CAA GCA GTG TGC GCC CCG AGC CGC GTT TCT TTC CTC ACT GGC AGG	409
101	Gln Gln Ala Val Cys Ala Pro Ser Arg Val Ser Phe Leu Thr Gly Arg	
102	80 85 90 95	
103		
104	AGA CCT GAC ACC ACC CGC CTG TAC GAC TTC AAC TCC TAC TGG AGG GTG	457
105	Arg Pro Asp Thr Thr Arg Leu Tyr Asp Phe Asn Ser Tyr Trp Arg Val	
106	100 105 110	
107		
108	CAC GCT GGA AAC TTC TCC ACC ATC CCC CAG TAC TTC AAG GAG AAT GGC	505
109	His Ala Gly Asn Phe Ser Thr Ile Pro Gln Tyr Phe Lys Glu Asn Gly	
110	115 120 125	
111		
112	TAT GTG ACC ATG TCG GTG GGA AAA GTC TTT CAC CCT GGG ATA TCT TCT	553
113	Tyr Val Thr Met Ser Val Gly Lys Val Phe His Pro Gly Ile Ser Ser	
114	130 135 140	
115		
116	AAC CAT ACC GAT GAT TCT CCG TAT AGC TGG TCT TTT CCA CCT TAT CAT	601
117	Asn His Thr Asp Asp Ser Pro Tyr Ser Trp Ser Phe Pro Pro Tyr His	
118	145 150 155	
119		
120	CCT TCC TCT GAG AAG TAT GAA AAC ACT AAG ACA TGT CGA GGG CCA GAT	649
121	Pro Ser Ser Glu Lys Tyr Glu Asn Thr Lys Thr Cys Arg Gly Pro Asp	
122	160 165 170 175	
123		
124	GGA GAA CTC CAT GCC AAC CTG CTT TGC CCT GTG GAT GTG CTG GAT GTT	697
125	Gly Glu Leu His Ala Asn Leu Leu Cys Pro Val Asp Val Leu Asp Val	
126	180 185 190	
127		
128	CCC GAG GGC ACC TTG CCT GAC AAA CAG AGC ACT GAG CAA GCC ATA CAG	745
129	Pro Glu Gly Thr Leu Pro Asp Lys Gln Ser Thr Glu Gln Ala Ile Gln	
130	195 200 205	
131		
132	TTG TTG GAA AAG ATG AAA ACG TCA GCC AGT CCT TTC TTC CTG GCC GTT	793
133	Leu Leu Glu Lys Met Lys Thr Ser Ala Ser Pro Phe Phe Leu Ala Val	
134	210 215 220	
135		
136	GGG TAT CAT AAG CCA CAC ATC CCC TTC AGA TAC CCC AAG GAA TTT CAG	841
137	Gly Tyr His Lys Pro His Ile Pro Phe Arg Tyr Pro Lys Glu Phe Gln	
138	225 230 235	
139		
140	AAG TTG TAT CCC TTG GAG AAC ATC ACC CTG GCC CCC GAT CCC GAG GTC	889
141	Lys Leu Tyr Pro Leu Glu Asn Ile Thr Leu Ala Pro Asp Pro Glu Val	
142	240 245 250 255	
143		
144	CCT GAT GGC CTA CCC CCT GTG GCC TAC AAC CCC TGG ATG GAC ATC AGG	937
145	Pro Asp Gly Leu Pro Pro Val Ala Tyr Asn Pro Trp Met Asp Ile Arg	
146	260 265 270	
147		
148	CAA CGG GAA GAC GTC CAA GCC TTA AAC ATC AGT GTG CCG TAT GGT CCA	985
149	Gln Arg Glu Asp Val Gln Ala Leu Asn Ile Ser Val Pro Tyr Gly Pro	
150	275 280 285	
151		
152	ATT CCT GTG GAC TTT CAG CGG AAA ATC CGC CAG AGC TAC TTT GCC TCT	1033

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153	Ile Pro Val Asp Phe Gln Arg Lys Ile Arg Gln Ser Tyr Phe Ala Ser			
154	290	295	300	
155				
156	GTG TCA TAT TTG GAT ACA CAG GTC GGC CGC CTC TTG AGT GCT TTG GAC	1081		
157	Val Ser Tyr Leu Asp Thr Gln Val Gly Arg Leu Leu Ser Ala Leu Asp			
158	305	310	315	
159				
160	GAT CTT CAG CTG GCC AAC AGC ACC ATC ATT GCA TTT ACC TCG GAT CAT	1129		
161	Asp Leu Gln Leu Ala Asn Ser Thr Ile Ile Ala Phe Thr Ser Asp His			
162	320	325	330	335
163				
164	GGG TGG GCT CTA GGT GAA CAT GGA GAA TGG GCC AAA TAC AGC AAT TTT	1177		
165	Gly Trp Ala Leu Gly Glu His Gly Glu Trp Ala Lys Tyr Ser Asn Phe			
166	340	345	350	
167				
168	GAT GTT GCT ACC CAT GTT CCC CTG ATA TTC TAT GTT CCT GGA AGG ACG	1225		
169	Asp Val Ala Thr His Val Pro Leu Ile Phe Tyr Val Pro Gly Arg Thr			
170	355	360	365	
171				
172	GCT TCA CTT CCG GAG GCA GGC GAG AAG CTT TTC CCT TAC CTC GAC CCT	1273		
173	Ala Ser Leu Pro Glu Ala Gly Glu Lys Leu Phe Pro Tyr Leu Asp Pro			
174	370	375	380	
175				
176	TTT GAT TCC GCC TCA CAG TTG ATG GAG CCA GGC AGG CAA TCC ATG GAC	1321		
177	Phe Asp Ser Ala Ser Gln Leu Met Glu Pro Gly Arg Gln Ser Met Asp			
178	385	390	395	
179				
180	CTT GTG GAA CTT GTG TCT CTT TTT CCC ACG CTG GCT GGA CTT GCA GGA	1369		
181	Leu Val Glu Leu Val Ser Leu Phe Pro Thr Leu Ala Gly Leu Ala Gly			
182	400	405	410	415
183				
184	CTG CAG GTT CCA CCT CGC TGC CCC GTT CCT TCA TTT CAC GTT GAG CTG	1417		
185	Leu Gln Val Pro Pro Arg Cys Pro Val Pro Ser Phe His Val Glu Leu			
186	420	425	430	
187				
188	TGC AGA GAA GGC AAG AAC CTT CTG AAG CAT TTT CGA TTC CGT GAC TTG	1465		
189	Cys Arg Glu Gly Lys Asn Leu Leu Lys His Phe Arg Phe Arg Asp Leu			
190	435	440	445	
191				
192	GAA GAG GAT CCG TAC CTC CCT GGT AAT CCC CGT GAA CTG ATT GCC TAT	1513		
193	Glu Glu Asp Pro Tyr Leu Pro Gly Asn Pro Arg Glu Leu Ile Ala Tyr			
194	450	455	460	
195				
196	AGC CAG TAT CCC CGG CCT TCA GAC ATC CCT CAG TGG AAT TCT GAC AAG	1561		
197	Ser Gln Tyr Pro Arg Pro Ser Asp Ile Pro Gln Trp Asn Ser Asp Lys			
198	465	470	475	
199				
200	CCG AGT TTA AAA GAT ATA AAG ATC ATG GGC TAT TCC ATA CGC ACC ATA	1609		
201	Pro Ser Leu Lys Asp Ile Lys Ile Met Gly Tyr Ser Ile Arg Thr Ile			
202	480	485	490	495
203				
204	GAC TAT AGG TAT ACT GTG TGG GTT GGC TTC AAT CCT GAT GAA TTT CTA	1657		
205	Asp Tyr Arg Tyr Thr Val Trp Val Gly Phe Asn Pro Asp Glu Phe Leu			

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206	500	505	510	
207				
208	GCT AAC TTT TCT GAC ATC CAT GCA GGG GAA CTG TAT TTT GTG GAT TCT			1705
209	Ala Asn Phe Ser Asp Ile His Ala Gly Glu Leu Tyr Phe Val Asp Ser			
210	515	520	525	
211				
212	GAC CCA TTG CAG GAT CAC AAT ATG TAT AAT GAT TCC CAA GGT GGA GAT			1753
213	Asp Pro Leu Gln Asp His Asn Met Tyr Asn Asp Ser Gln Gly Gly Asp			
214	530	535	540	
215				
216	CTT TTC CAG TTG TTG ATG CCT TGAGTTTGC CAACCATGGA TGGCAAATGT			1804
217	Leu Phe Gln Leu Leu Met Pro			
218	545	550		
219				
220	GATGTGCTCC CTTCCAGCTG GTGAGAGGAG GAGTTAGAGC TGGTCGTTT GTGATTACCC			1864
221				
222	ATAATATTGG AAGCAGCCTG AGGGCTAGTT AATCCAAACA TGCATCAACA ATTTGCCCTG			1924
223				
224	AGAATATGTA ACAGCCAAAC CTTTCGTTT AGTCTTATT AAAATTATA ATTGGTAATT			1984
225				
226	GGACCAGTTT TTTTTTAAT TTCCCTCTTT TTAAAACAGT TACGGCTTAT TTACTGAATA			2044
227				
228	AATACAAAGC AAACAAACTC AAGTTATGTC ATACCTTG G ATACGAAGAC CATACTATAAT			2104
229				
230	AACCAAACAT AACATTATAC ACAAGAATA CTTTCATTAT TTGTGGAATT TAGTGCATT			2164
231				
232	CAAAAAGTAA TCATATATCA AACTAGGCAC CACACTAAGT TCCTGATTAT TTTGTTATA			2224
233				
234	ATTTAATAAT ATATCTTATG AGCCCTATAT ATTCAAAATA TTATGTTAAC ATGTAATCCA			2284
235				
236	TGTTTCTTT TCC			2297
237				

## 238 (2) INFORMATION FOR SEQ ID NO:2:

## 239 (i) SEQUENCE CHARACTERISTICS:

- |     |                               |  |
|-----|-------------------------------|--|
| 240 | (i) SEQUENCE CHARACTERISTICS: |  |
| 241 |                               |  |
| 242 | (A) LENGTH: 550 amino acids   |  |
| 243 | (B) TYPE: amino acid          |  |
| 244 | (D) TOPOLOGY: linear          |  |
| 245 |                               |  |

## 246 (ii) MOLECULE TYPE: protein

## 247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

249				
250	Met Pro Pro Pro Arg Thr Gly Arg Gly Leu Leu Trp Leu Gly Leu Val			
251	1	5	10	15
252				
253	Leu Ser Ser Val Cys Val Ala Leu Gly Ser Glu Thr Gln Ala Asn Ser			
254	20	25	30	
255				
256	Thr Thr Asp Ala Leu Asn Val Leu Leu Ile Ile Val Asp Asp Leu Arg			
257	35	40	45	
258				

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